



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,066

DATE: 04/26/2002

TIME: 14:29:50

Input Set : N:\Crf3\RULE60\10017066.raw

Output Set: N:\CRF3\04262002\J017066.raw

ENTERED

```

1 <110> APPLICANT: Arthur B. Raitano
2   Daniel E.H. Afar
3   Aya Jakobovits
4   Mary Faris
5   Rene S. Hubert
6   Steve Chappell Mitchell
7   Douglas C. Saffran
8 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
9   UP-REGULATED IN PROSTATE CANCER AND USES THEREOF
10 <130> FILE REFERENCE: 129.24USU1
11 <140> CURRENT APPLICATION NUMBER: 10/017,066
12 <141> CURRENT FILING DATE: 2001-12-14
13 <150> PRIOR APPLICATION NUMBER: US/09/680,728
14 <151> PRIOR FILING DATE: 2000-10-05
15 <160> NUMBER OF SEQ ID NOS: 50
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 3136
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo Sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (133)...(1083)
25 <400> SEQUENCE: 1
26   cagagaggct gtatttcagt gcagcctgcc agacctcttc tggaggaaga ctggacaaag      60
27   ggggtcacac attccttcca tacggttgag cctctacctg cctggtgctg gtcacagttc      120
28   agcttcttca tg atg gtg gat ccc aat ggc aat gaa tcc agt gct aca tac      171
29   Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr
30   1           5           10
31   ttc atc cta ata ggc ctc cct ggt tta gaa gag gct cag ttc tgg ttg      219
32   Phe Ile Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu
33   15           20           25
34   gcc ttc cca ttg tgc tcc ctc tac ctt att gct gtg cta ggt aac ttg      267
35   Ala Phe Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu
36   30           35           40           45
37   aca atc atc tac att gtg cgg act gag cac agc ctg cat gag ccc atg      315
38   Thr Ile Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met
39   50           55           60
40   tat ata ttt ctt tgc atg ctt tca ggc att gac atc ctc atc tcc acc      363
41   Tyr Ile Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr
42   65           70           75
43   tca tcc atg ccc aaa atg ctg gcc atc ttc tgg ttc aat tcc act acc      411
44   Ser Ser Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr

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45	80							85							90							
46	atc	cag	ttt	gat	gct	tgt	ctg	cta	cag	att	ttt	gcc	atc	cac	tcc	tta	459					
47	Ile	Gln	Phe	Asp	Ala	Cys	Leu	Leu	Gln	Ile	Phe	Ala	Ile	His	Ser	Leu						
48	95						100						105									
49	tct	ggc	atg	gaa	tcc	aca	gtg	ctg	ctg	gcc	atg	gct	ttt	gac	cgc	tat	507					
50	Ser	Gly	Met	Glu	Ser	Thr	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr						
51	110					115					120					125						
52	gtg	gcc	atc	tgt	cac	cca	ctg	cgc	cat	gcc	aca	gta	ctt	acg	ttg	cct	555					
53	Val	Ala	Ile	Cys	His	Pro	Leu	Arg	His	Ala	Thr	Val	Leu	Thr	Leu	Pro						
54	130						135						140									
55	cgt	gtc	acc	aaa	att	ggg	gtg	gct	gct	gtg	gtg	cgg	ggg	gct	gca	ctg	603					
56	Arg	Val	Thr	Lys	Ile	Gly	Val	Ala	Ala	Val	Val	Arg	Gly	Ala	Ala	Leu						
57	145						150						155									
58	atg	gca	ccc	ctt	cct	gtc	ttc	atc	aag	cag	ctg	ccc	ttc	tgc	cgc	tcc	651					
59	Met	Ala	Pro	Leu	Pro	Val	Phe	Ile	Lys	Gln	Leu	Pro	Phe	Cys	Arg	Ser						
60	160						165						170									
61	aat	atc	ctt	tcc	cat	tcc	tac	tgc	cta	cac	caa	gat	gtc	atg	aag	ctg	699					
62	Asn	Ile	Leu	Ser	His	Ser	Tyr	Cys	Leu	His	Gln	Asp	Val	Met	Lys	Leu						
63	175						180						185									
64	gcc	tgt	gat	gat	atc	cgg	gtc	aat	gtc	gtc	tat	ggc	ctt	atc	gtc	atc	747					
65	Ala	Cys	Asp	Asp	Ile	Arg	Val	Asn	Val	Val	Tyr	Gly	Leu	Ile	Val	Ile						
66	190					195					200					205						
67	atc	tcc	gcc	att	ggc	ctg	gac	tca	ctt	ctc	atc	tcc	ttc	tca	tat	ctg	795					
68	Ile	Ser	Ala	Ile	Gly	Leu	Asp	Ser	Leu	Leu	Ile	Ser	Phe	Ser	Tyr	Leu						
69	210						215						220									
70	ctt	att	ctt	aag	act	gtg	ttg	ggc	ttg	aca	cgt	gaa	gcc	cag	gcc	aag	843					
71	Leu	Ile	Leu	Lys	Thr	Val	Leu	Gly	Leu	Thr	Arg	Glu	Ala	Gln	Ala	Lys						
72	225						230						235									
73	gca	ttt	ggc	act	tgc	gtc	tct	cat	gtg	tgt	gct	gtg	ttc	ata	ttc	tat	891					
74	Ala	Phe	Gly	Thr	Cys	Val	Ser	His	Val	Cys	Ala	Val	Phe	Ile	Phe	Tyr						
75	240						245						250									
76	gta	cct	ttc	att	gga	ttg	tcc	atg	gtg	cat	cgc	ttt	agc	aag	cgg	cgt	939					
77	Val	Pro	Phe	Ile	Gly	Leu	Ser	Met	Val	His	Arg	Phe	Ser	Lys	Arg	Arg						
78	255						260						265									
79	gac	tct	ccg	ctg	ccc	gtc	atc	ttg	gcc	aat	atc	tat	ctg	ctg	gtt	cct	987					
80	Asp	Ser	Pro	Leu	Pro	Val	Ile	Leu	Ala	Asn	Ile	Tyr	Leu	Leu	Val	Pro						
81	270					275					280					285						
82	cct	gtg	ctc	aac	cca	att	gtc	tat	gga	gtg	aag	aca	aag	gag	att	cga	1035					
83	Pro	Val	Leu	Asn	Pro	Ile	Val	Tyr	Gly	Val	Lys	Thr	Lys	Glu	Ile	Arg						
84	290						295						300									
85	cag	cgc	atc	ctt	cga	ctt	ttc	cat	gtg	gcc	aca	cac	gct	tca	gag	ccc	1083					
86	Gln	Arg	Ile	Leu	Arg	Leu	Phe	His	Val	Ala	Thr	His										

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Input Set : N:\Crif3\RULE60\10017066.raw

Output Set: N:\CRF3\04262002\J017066.raw

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94  aacacagaat ataataaaat gagataatct agcttaaaac tataacttcc tcttcagaac 1503
95  tcccaaccac attggatctc agaaaaatgc tgtcttcaaa atgacttcta cagagaagaa 1563
96  ataatttttc ctctggacac tagcacttaa ggggaagatt ggaagtaaag ccttgaaaag 1623
97  agtacattta cctacgttaa tgaaagtga cacactgttc tgagagtttt cacagcatat 1683
98  ggacctgttt ttctctatct aattttctta tcaacccttt aattaggcaa agatattatt 1743
99  agtacctca ttgtagccat gggaaaattg atgttcagtg gggatcagtg aattaaatgg 1803
100 ggtcatacaa gtataaaaat taaaaaaaaa aaagacttca tgcccaatct catatgatgt 1863
101 ggaagaactg ttagagagac caacagggtg gtgggttaga gatttcaga gtcttacatt 1923
102 ttctagagga ggtatttaat ttcttctcac tcatccagtg ttgtatttag gaatttcctg 1983
103 gcaacagAAC tcatggcttt aatcccacta gctattgctt attgtcctgg tccaattgcc 2043
104 aattacctgt gtcttgaag aagtgatttc taggttcacc attatggaag attcttattc 2103
105 agaaagtctg catagggctt atagcaagtt atttattttt aaaagttcca taggtgattc 2163
106 tgataggcag tgaggttagg gagccaccag ttatgatggg aagtatggaa tggcaggtct 2223
107 tgaagataac attggccttt tgagtgtgac tcgtagctgg aaagtgaggg aatcttcagg 2283
108 accatgcttt atttggggct ttgtgcagta tggaacaggg actttgagac caggaaagca 2343
109 atctgactta ggcattggaa tcaggcatct ttgtctctga ggggctatta ccaagggtta 2403
110 ataggtttca tcttcaacag gatatgacaa cagtgttaac caagaaactc aaattacaaa 2463
111 tactaaaaca tgtgatcata tatgtggtta gtttcatttt ctttttcaat cctcaggttc 2523
112 cctgatattg attcctataa catgctttca tccccttttg taatggatat catatttgga 2583
113 aatgcctatt taatacttgt atttgcctgt ggactgtaag cccatgaggg cactgtttat 2643
114 tattgaatgt catctctgtt catcattgac tgctctttgc tcatcattga atccccagc 2703
115 aaagtgccta gaacataata gtgcttatgc ttgacaccgg ttatttttca tcaaacctga 2763
116 ttccttctgt cctgaacaca tagccaggca attttccagc cttctttgag ttgggtatta 2823
117 ttaaatcttg gccattactt ccaatgtgag tggaagtga atgtgcaatt tctatacctg 2883
118 gctcataaaa cctcccatg tgcagccttt catgttgaca ttaaagtga cttgggaagc 2943
119 tatgtgttac acagagtaa tcaccagaag cctggatttc tgaaaaaact gtgcagagcc 3003
120 aaacctctgt catttgcaac tcccacttgt atttgcacga ggcagttgga taagtgaaaa 3063
121 ataaagtact atttgttcaa gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3123
122 aaaaaaaaaa aaa 3136
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 317
126 <212> TYPE: PRT
127 <213> ORGANISM: Homo Sapiens
128 <400> SEQUENCE: 2
129 Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile Leu
130 1 5 10 15
131 Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe Pro
132 20 25 30
133 Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile Ile
134 35 40 45
135 Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
136 50 55 60
137 Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser Met
138 65 70 75 80
139 Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe
140 85 90 95
141 Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu Ser Gly Met
142 100 105 110
143 Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile

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```

144          115          120          125
145 Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr
146          130          135          140
147 Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala Pro
148          145          150          155          160
149 Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu
150          165          170          175
151 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp
152          180          185          190
153 Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser Ala
154          195          200          205
155 Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile Leu
156          210          215          220
157 Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe Gly
158          225          230          235          240
159 Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro Phe
160          245          250          255
161 Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro
162          260          265          270
163 Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val Leu
164          275          280          285
165 Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg Ile
166          290          295          300
167 Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
168          305          310          315
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 320
172 <212> TYPE: PRT
173 <213> ORGANISM: Rat Protein
174 <400> SEQUENCE: 3
175 Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Met Leu Ile Gly Ile
176 1 5 10 15
177 Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser
178 20 25 30
179 Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
180 35 40 45
181 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
182 50 55 60
183 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
184 65 70 75 80
185 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
186 85 90 95
187 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
188 100 105 110
189 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
190 115 120 125
191 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
192 130 135 140
193 Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu

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Input Set : N:\Crf3\RULE60\10017066.raw

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```

194      145      150      155      160
195      Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
196                      165                      170                      175
197      Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
198                      180                      185                      190
199      Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
200                      195                      200                      205
201      Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
202                      210                      215                      220
203      Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
204      225                      230                      235                      240
205      Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
206                      245                      250                      255
207      Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
208                      260                      265                      270
209      Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
210                      275                      280                      285
211      Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
212      290                      295                      300
213      Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
214      305                      310                      315                      320
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 320
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo Sapiens
220 <400> SEQUENCE: 4
221      Met Ser Ser Cys Asn Phe Thr His Ala Thr Cys Val Leu Ile Gly Ile
222      1                      5                      10                      15
223      Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
224                      20                      25                      30
225      Met Tyr Val Val Ala Met Cys Gly Asn Cys Ile Val Val Phe Ile Val
226                      35                      40                      45
227      Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
228                      50                      55                      60
229      Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
230      65                      70                      75                      80
231      Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Ile Glu Ala Cys
232                      85                      90                      95
233      Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
234                      100                     105                     110
235      Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
236                      115                     120                     125
237      Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
238      130                     135                     140
239      Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
240      145                     150                     155                     160
241      Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
242                      165                      170                      175
243      Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/017,066

DATE: 04/26/2002  
TIME: 14:29:51

Input Set : N:\Crf3\RULE60\10017066.raw  
Output Set: N:\CRF3\04262002\J017066.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:41; N Pos. 6,12,15  
Seq#:42; N Pos. 3,6,12,15  
Seq#:43; N Pos. 12,15  
Seq#:44; N Pos. 3,12,15  
Seq#:45; N Pos. 3,9,18  
Seq#:46; N Pos. 3,9  
Seq#:47; N Pos. 6,9,21  
Seq#:48; N Pos. 1,13,16  
Seq#:49; N Pos. 1,7,10,16  
Seq#:50; N Pos. 10,16,19

## VERIFICATION SUMMARY

DATE: 04/26/2002

PATENT APPLICATION: US/10/017,066

TIME: 14:29:51

Input Set : N:\Crif3\RULE60\10017066.raw

Output Set: N:\CRF3\04262002\J017066.raw

L:630 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:633 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:41  
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0  
L:642 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:645 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:42  
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0  
L:654 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:657 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:43  
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0  
L:666 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:669 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:44  
L:670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0  
L:678 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:681 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:45  
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0  
L:690 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:693 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46  
L:694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0  
L:702 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:705 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:47  
L:706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0  
L:714 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:717 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:48  
L:718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0  
L:726 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:729 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:49  
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0  
L:738 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:741 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:50  
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0